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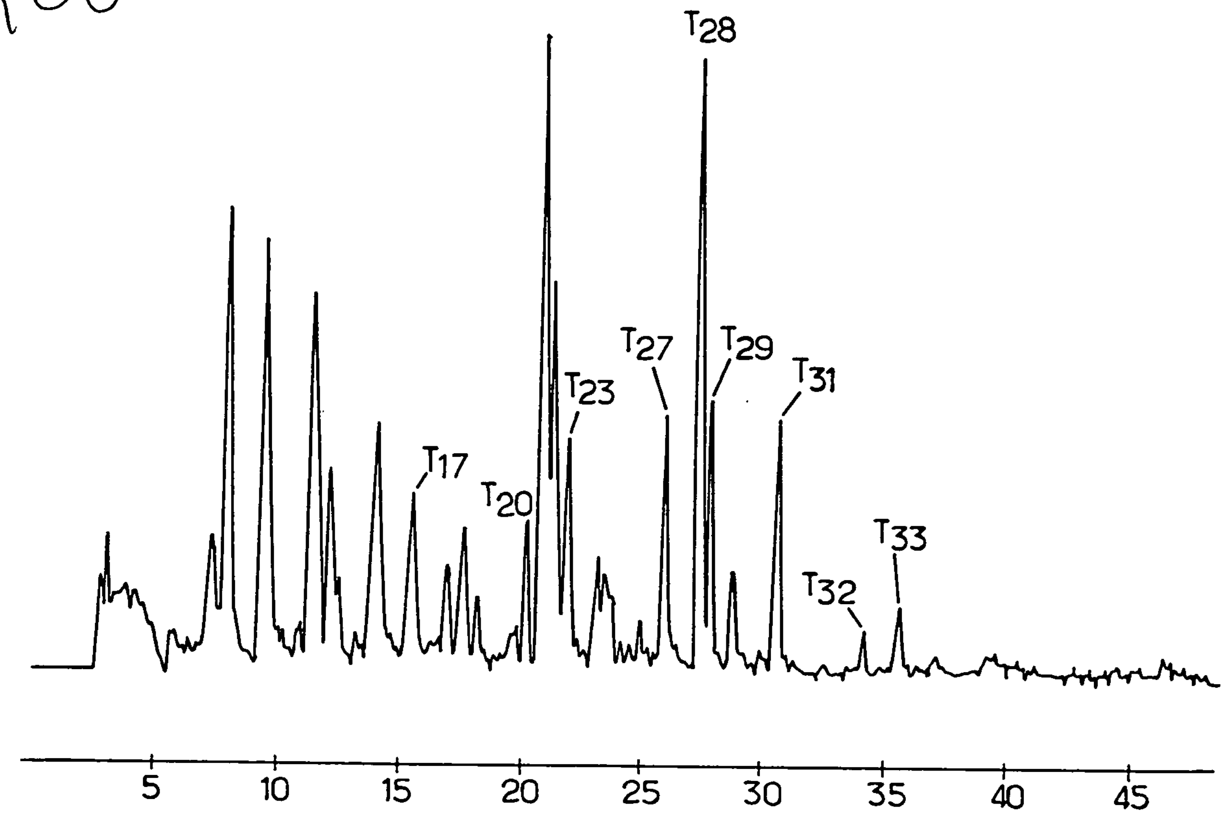

FIG. 1

Elution profile by measurement of the optical density at 218 nm of the product of tryptic digestion of urate oxidase

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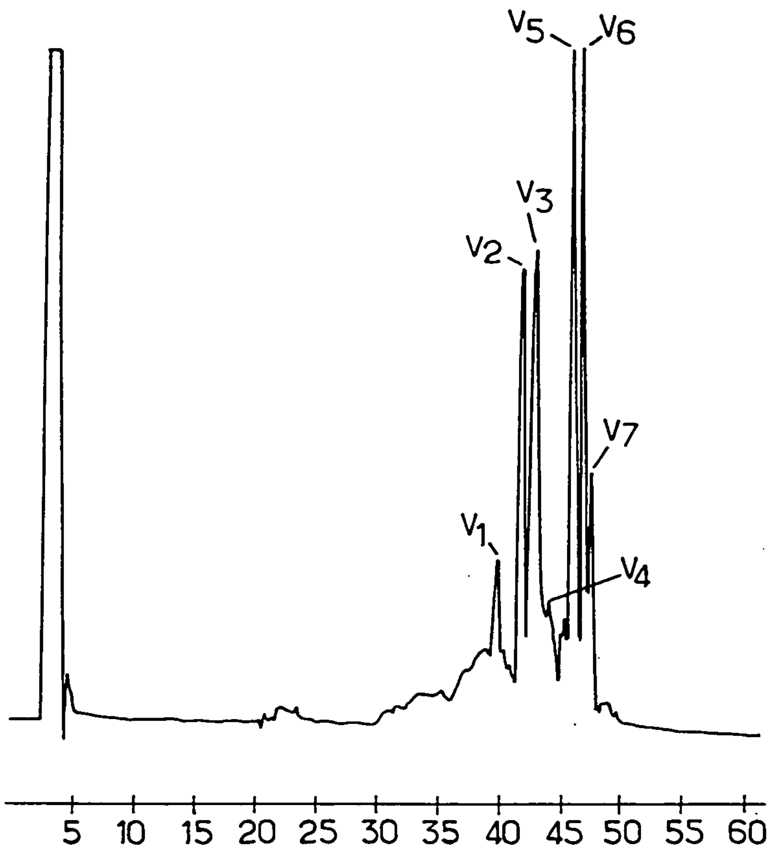

FIG. 2

Elution profile by measurement of the optical density at 218 nm of the product of digestion of urate oxidase with protease V8

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```
   1  AAACCCTCACTGCCTCTCTCATTCCTTCCG GTGCCCCCGATCCTCAATCCAACTTGTACA   60
  61  TACTTCTCCCAACTCTCTGCTATATCCTTC ATATTCCCATACTACAAGATGTCCGCAGTA  120
 121  AAAGCAGCCCGCTACGGCAAGGACAATGTC CGCGTCTACAAGGTTCACAAGGACGAGAAG  180
 181  ACCGGTGTCCAGACGGTGTACGAGATGACC GTCTGTGTGCTTCTGGAGGGTGAGATTGAG  240
 241  ACCTCTTACACCAAGGCCGACAACAGCGTC ATTGTCGCAACCGACTCCATTAAGAACACC  300
      ↓
 301  ATTTACATCACCGCCAAGCAGAACCCCGTT ACTCCTCCCGAGCTGTTCGGCTCCATCCTG  360
 361  GGCACACACTTCATTGAGAAGTACAACCAC ATCCATGCCGCTCACGTCAACATTGTCTGC  420
 421  CACCGCTGGACCCGGATGGACATTGACGGC AAGCCACACCCTCACTCCTTCATCCGCGAC  480
                                A*
 481  AGCGAGGAGAAGCGGAATGTGCAGGTGGAC GTGGTCGAGGGCAAGGGCATCGATATCAAG  540
 541  TCGTCTCTGTCCGGCCTGACCGTGCTGAAG AGCACCAACTCGCAGTTCTGGGGCTTCCTG  600
 601  CGTGACGAGTACACCACACTTAAGGAGACC TGGGACCGTATCCTGAGCACCGACGTCGAT  660
 661  GCCACTTGGCAGTGGAAGAATTTCAGTGGA CTCCAGGAGGTCCGCTCGCACGTGCCTAAG  720
 721  TTCGATGCTACCTGGGCCACTGCTCGCGAG GTCACTCTGAAGACTTTTGCTGAAGATAAC  780
 781  AGTGCCAGCGTGCAGGCCACTATGTACAAG ATGGCAGAGCAAATCCTGGCGCGCCAGCAG  840
 841  CTGATCGAGACTGTCGAGTACTCGTTGCCT AACAAGCACTATTTCGAAATCGACCTGAGC  900
      G*
 901  TGGCACAAGGGCCTCCAAAACACCGGCAAG AACGCCGAGGTCTTCGCTCCTCAGTCGGAC  960
 961  CCCAACGGTCTGATCAAGTGTACCGTCGGC CGGTCCTCTCTGAAGTCTAAATTGTAAACC 1020
1021  AACATGATTCTCACGTTCCGGAGTTTCCAA GGCAAACTGTATATAGTCTGGGATAGGGTA 1080
1081  TAGCATTCATTCACTTGTTTTTACTTCCA AAAAAAAAAA...
```

FIG. 3

Nucleotide sequence of clone 9C and of part of clone 9A

↓ : start of clone 9A

```
109  ATGTCCGCAGTAAAAGCAGCCCGCTACGGC AAGGACAATGTCCGCGTCTACAAGGTTCAC  168
  1  MetSerAlaValLysAlaAlaArgTyrGly LysAspAsnValArgValTyrLysValHis   20

169  AAGGACGAGAAGACCGGTGTCCAGACGGTG TACGAGATGACCGTCTGTGTGCTTCTGGAG  228
 21  LysAspGluLysThrGlyValGlnThrVal TyrGluMetThrValCysValLeuLeuGlu   40

229  GGTGAGATTGAGACCTCTTACACCAAGGCC GACAACAGCGTCATTGTCGCAACCGACTCC  288
 41  GlyGluIleGluThrSerTyrThrLysAla AspAsnSerValIleValAlaThrAspSer   60
                                        V3
289  ATTAAGAACACCATTTACATCACCGCCAAG CAGAACCCCGTTACTCCTCCCGAGCTGTTC  348
 61  IleLysAsnThrIleTyrIleThrAlaLys GlnAsnProValThrProProGluLeuPhe   80
                                              T32/T33
349  GGCTCCATCCTGGGCACACACTTCATTGAG AAGTACAACCACATCCATGCCGCTCACGTC  408
 81  GlySerIleLeuGlyThrHisPheIleGlu LysTyrAsnHisIleHisAlaAlaHisVal  100

409  AACATTGTCTGCCACCGCTGGACCCGGATG GACATTGACGGCAAGCCACACCCTCACTCC  468
101  AsnIleValCysHisArgTrpThrArgMet AspIleAspGlyLysProHisProHisSer  120

469  TTCATCCGCGACAGCGAGGAGAAGCGGAAT GTGCAGGTGGACGTGGTCGAGGGCAAGGGC  528
121  PheIleArgAspSerGluGluLysArgAsn ValGlnValAspValValGluGlyLysGly  140
                                        T17
529  ATCGATATCAAGTCGTCTCTGTCCGGCCTG ACCGTGCTGAAGAGCACCAACTCGCAGTTC  588
141  IleAspIleLysSerSerLeuSerGlyLeu ThrValLeuLysSerThrAsnSerGlnPhe T31 160
                V5/V6
589  TGGGGCTTCCTGCGTGACGAGTACACCACA CTTAAGGAGACCTGGGACCGTATCCTGAGC  648
161  TrpGlyPheLeuArgAspGluTyrThrThr LeuLysGluThrTrpAspArgIleLeuSer  180

649  ACCGACGTCGATGCCACTTGGCAGTGGAAG AATTTCAGTGGACTCCAGGAGGTCCGCTCG  708
181  ThrAspValAspAlaThrTrpGlnTrpLys AsnPheSerGlyLeuGlnGluValArgSer  200
                T28                              T20
```

FIG. 4 (cont. next page)

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```
709   CACGTGCCTAAGTTCGATGCTACCTGGGCC ACTGCTCGCGAGGTCACTCTGAAGACTTTT   768
201   HisValProLysPheAspAlaThrTrpAla ThrAlaArgGluValThrLeuLysThrPhe   220
                      T23
769   GCTGAAGATAACAGTGCCAGCGTGCAGGCC ACTATGTACAAGATGGCAGAGCAAATCCTG   828
221   AlaGluAspAsnSerAlaSerValGlnAla ThrMetTyrLysMetAlaGluGlnIleLeu   240
                V2
829   GCGCGCCAGCAGCTGATCGAGACTGTCGAG TACTCGTTGCCTAACAAGCACTATTTCGAA   888
241   AlaArgGlnGlnLeuIleGluThrValGlu TyrSerLeuProAsnLysHisTyrPheGlu   260
                                                   T29/
                                                 V1
889   ATCGACCTGAGCTGGCACAAGGGCCTCCAA AACACCGGCAAGAACGCCGAGGTCTTCGCT   948
261   IleAspLeuSerTrpHisLysGlyLeuGln AsnThrGlyLysAsnAlaGluValPheAla   280
   T27
949   CCTCAGTCGGACCCCAACGGTCTGATCAAG TGTACCGTCGGCCGGTCCTCTCTGAAGTCT   1008
281   ProGlnSerAspProAsnGlyLeuIleLys CysThrValGlyArgSerSerLeuLysSer   300

1009  AAATTGTAA
301   LysLeuEnd
```

FIG.4 (contd.)

DNA sequence opened by ATG in position 109 in Figure 3 and polypeptide coded for.

The sequenced peptides obtained by hydrolysis of A. flavus urate oxidase with trypsin and protease V8 are shown by arrows opposite the polypeptide coded for, according to

⟷ : tryptic peptide

⟵ - - ⟶ : peptide obtained by hydrolysis with protease V8.

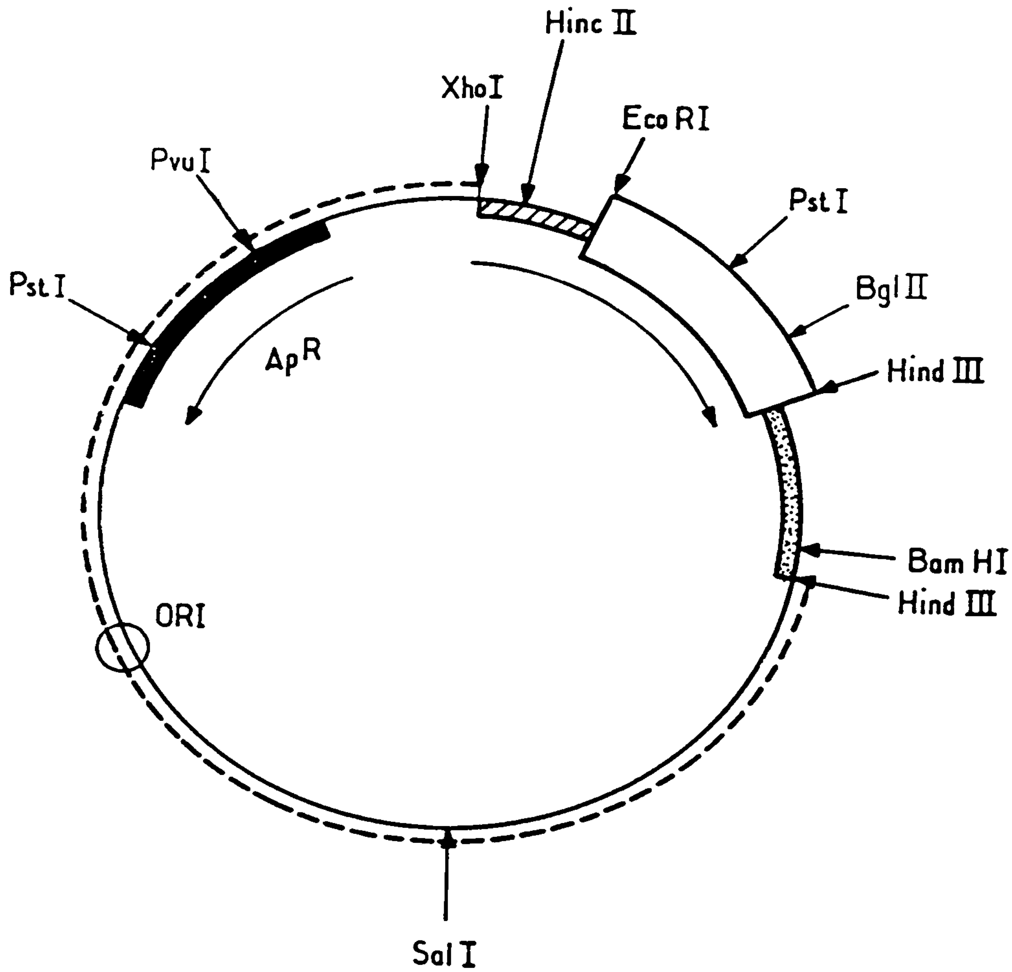

FIG.5

Plasmid p 163,1

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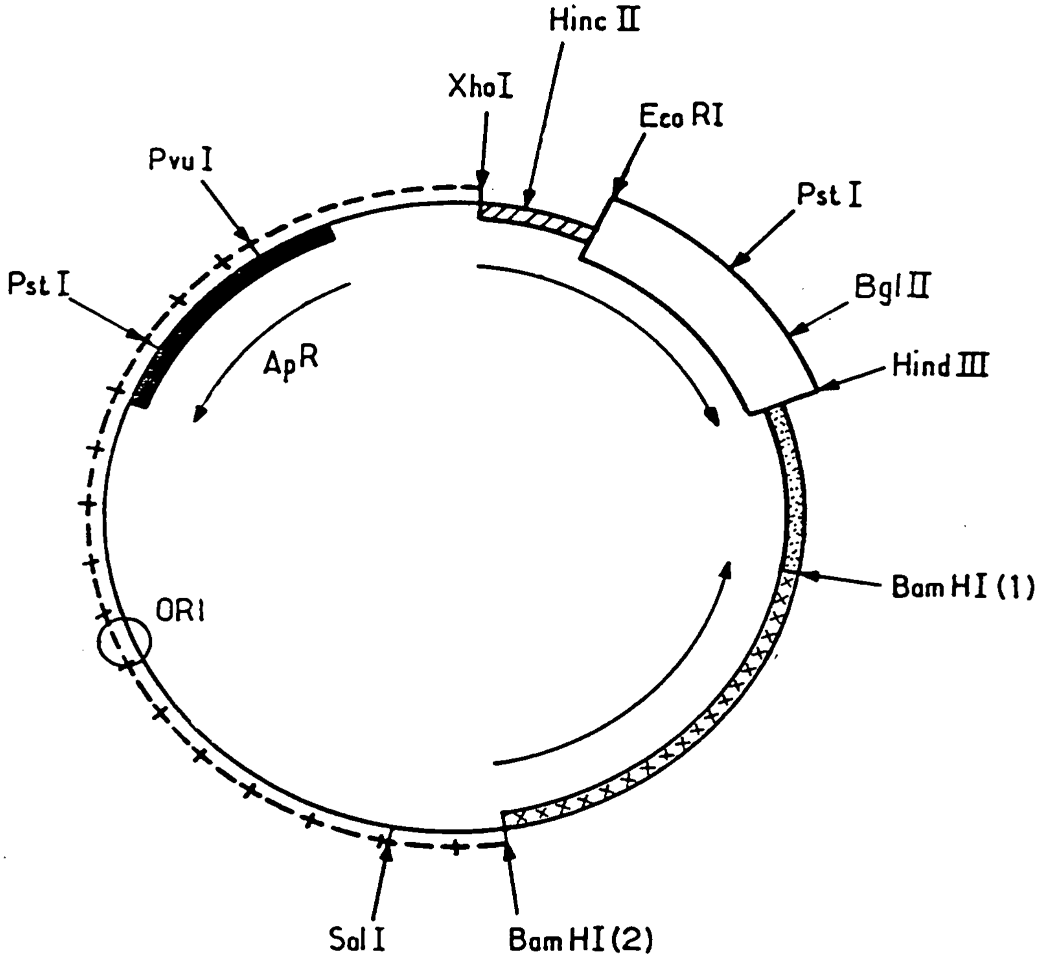

FIG. 6

Plasmid p 160

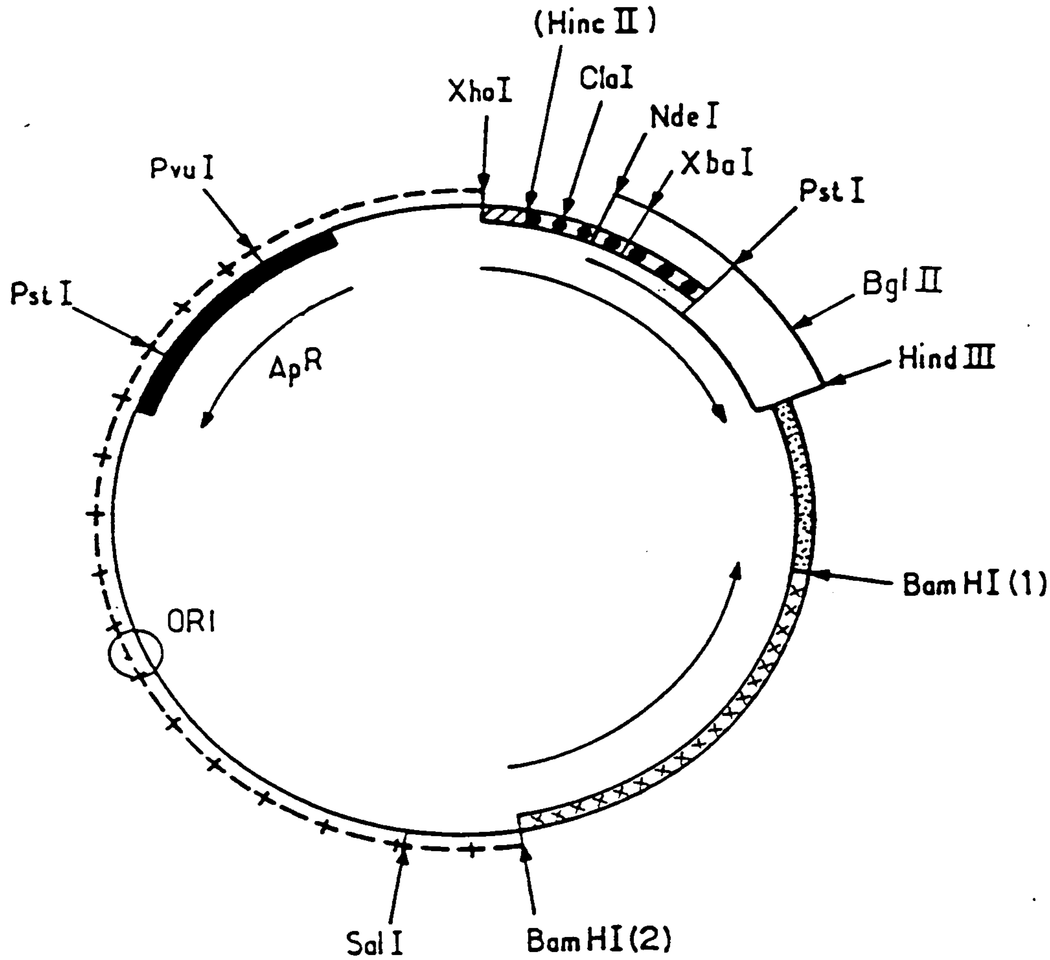

FIG. 7

Plasmid p 373,2

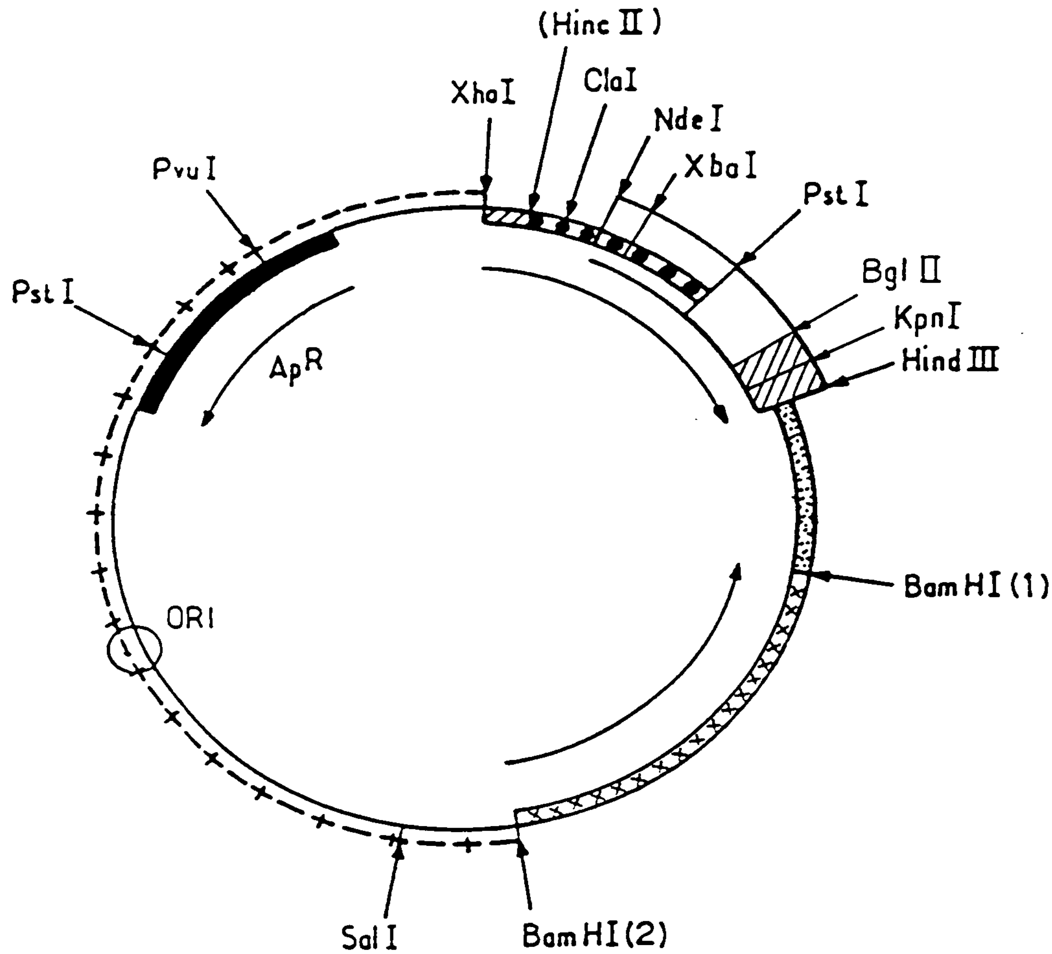

FIG.8

Plasmid p 462

07/659408

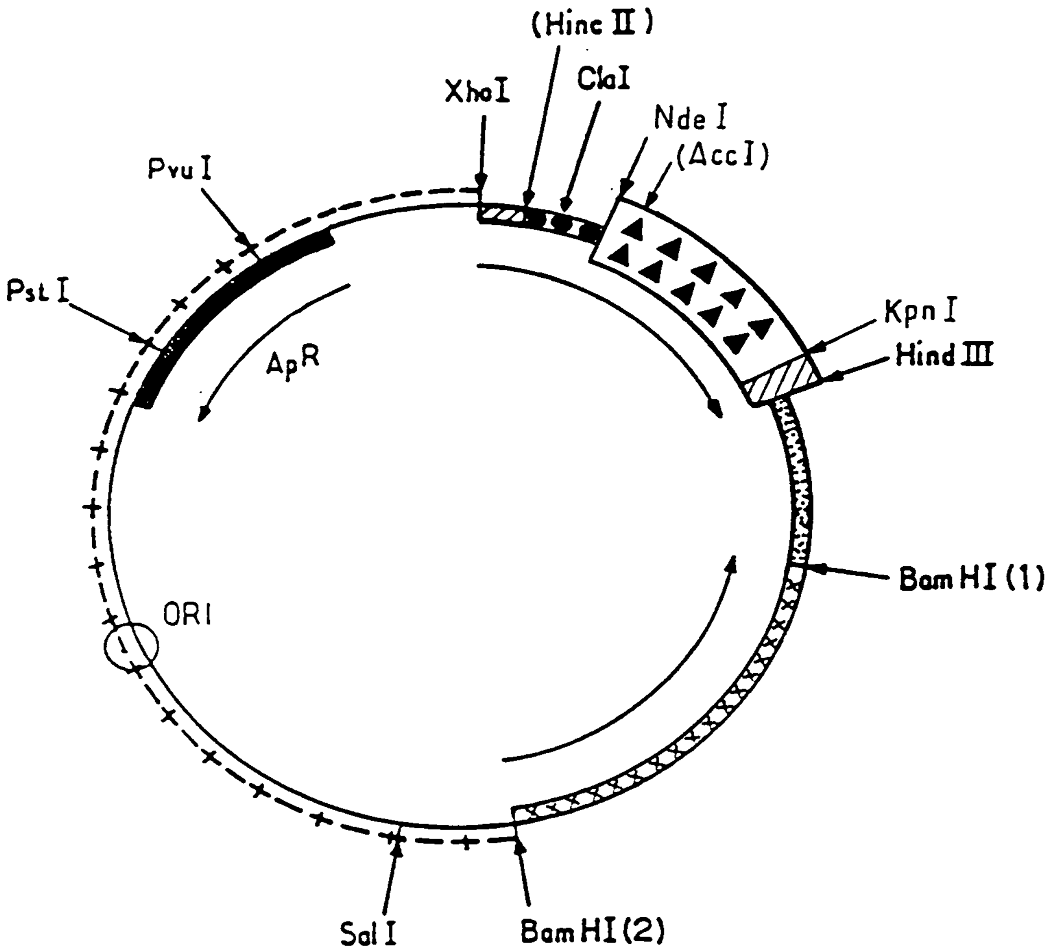

FIG. 9

Plasmid p 466

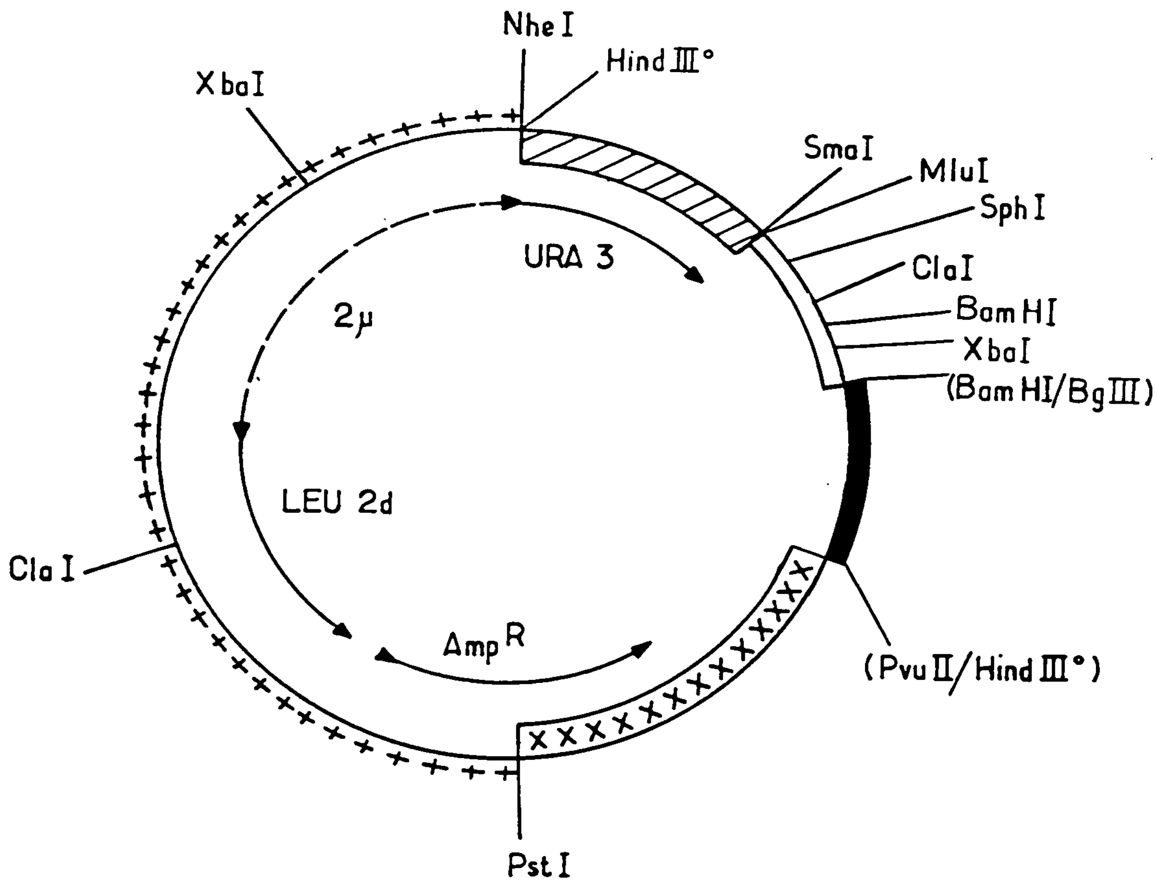

FIG.10

Plasmid pEMR 414

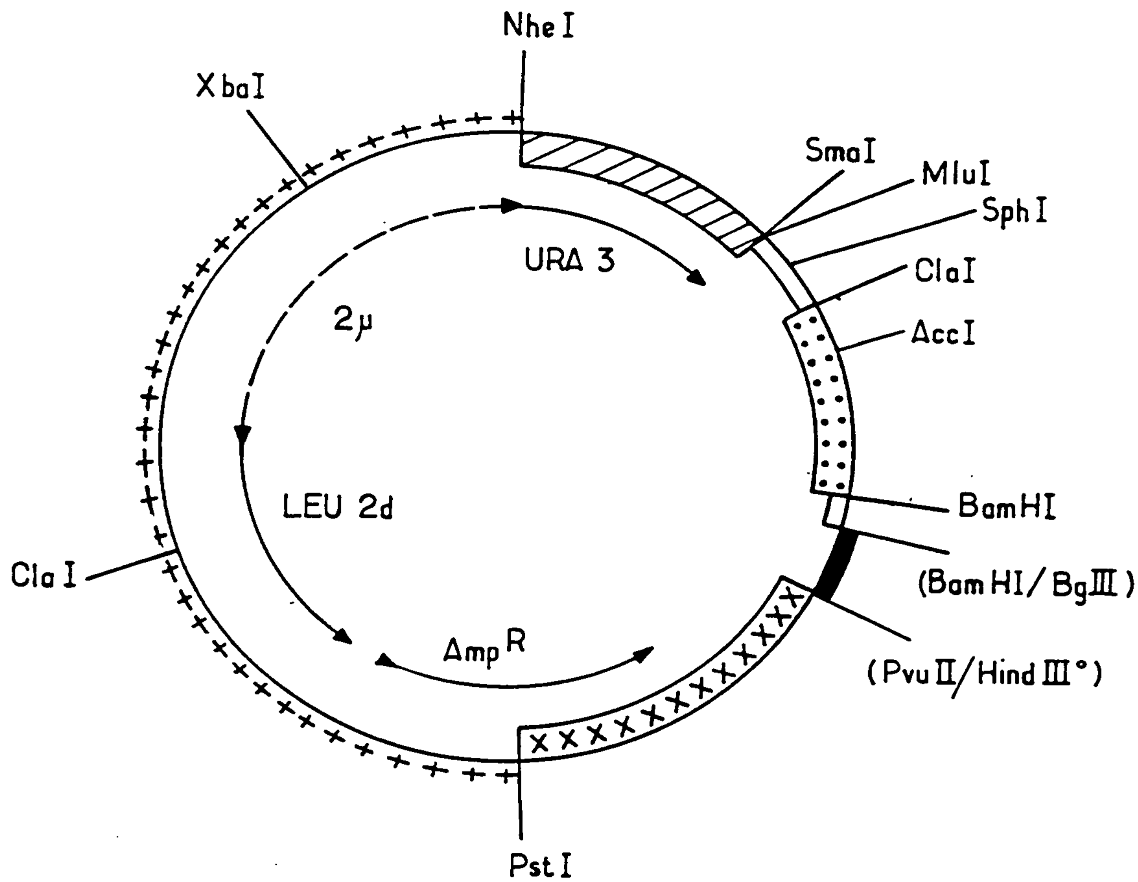

FIG.11

Plasmid pEMR 469

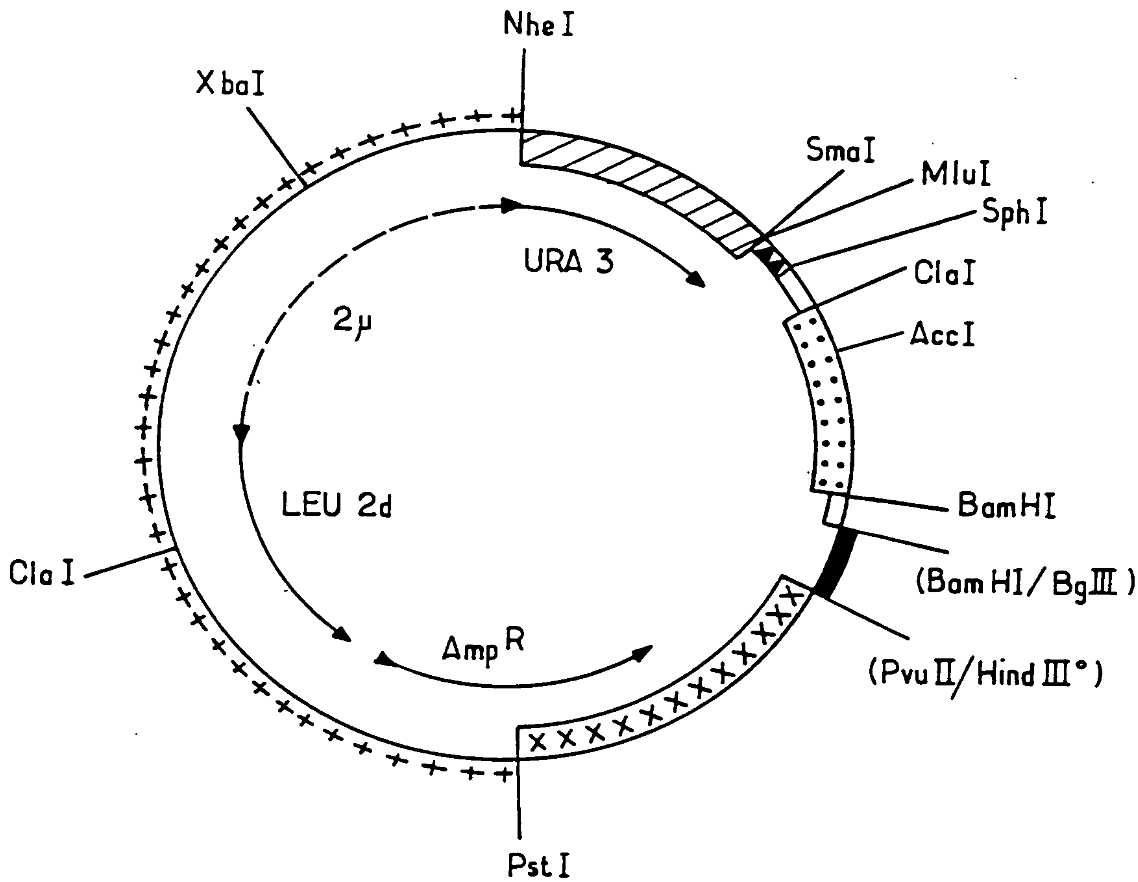

FIG.12

Plasmid pEMR 473

87/659408

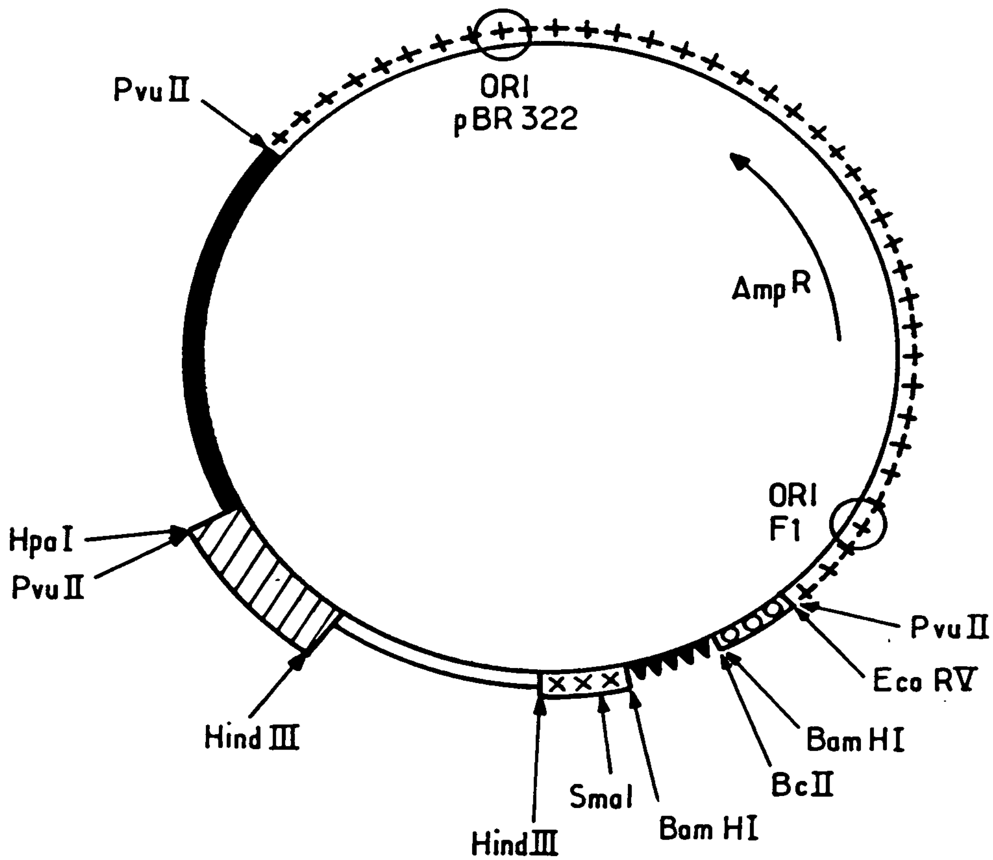

FIG.13

Plasmid PSE 1

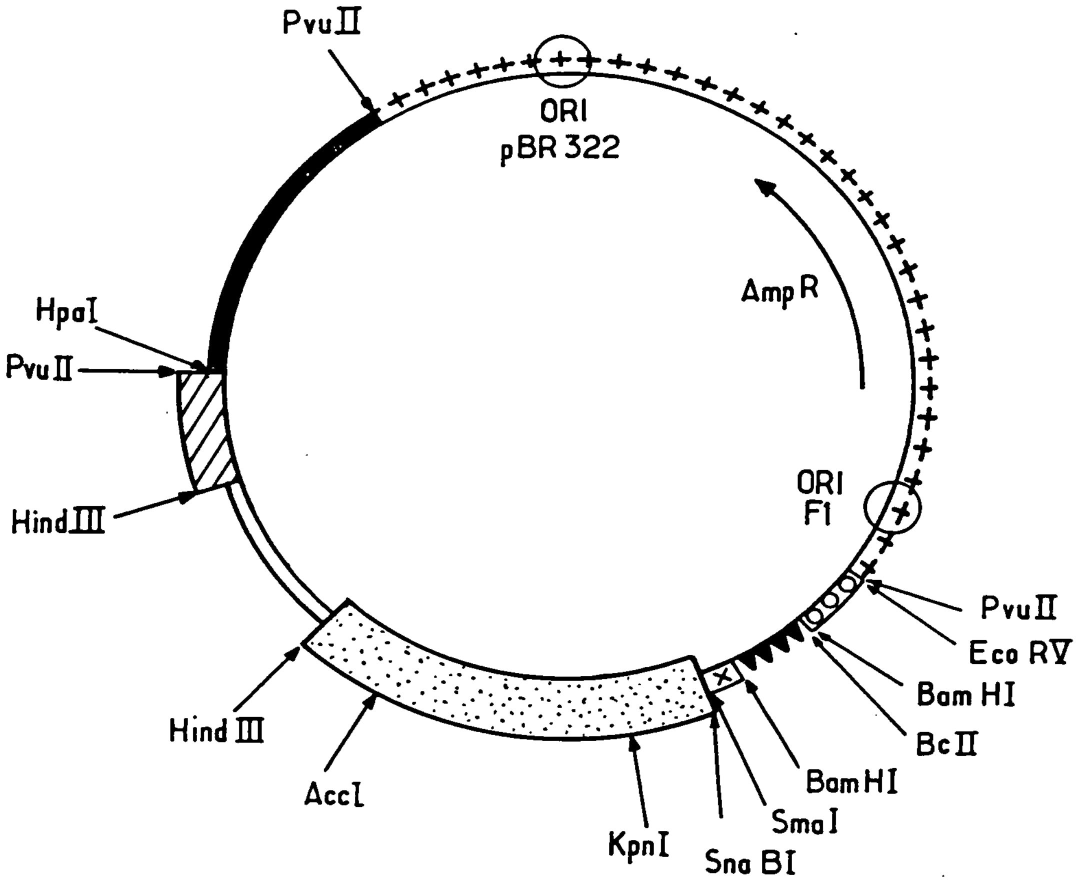

FIG.14

Plasmid pSV860